



Blast 2 Sequences results

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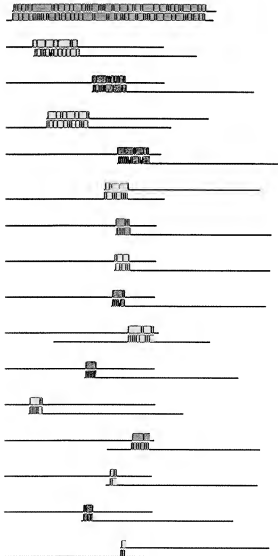
BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.18 [Mar-02-2008]

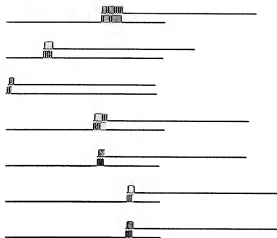
Matrix: gap open: gap extension:
x_dropoff: expect: wordsize: Filter ☒ View option:
Masking character option: ☒ for protein, n for nucleotide Masking color option:
☐ Show CDS translation

Sequence 1: gi|126012562|low density lipoprotein-related protein 1 [Homo sapiens]
Length = 4544 (1 .. 4544)

Sequence 2: gi|126012573|low density lipoprotein-related protein 2 [Homo sapiens]
>gi|160332309|sp|P98164.3|LRP2_HUMAN Low-density lipoprotein receptor-related protein 2 precursor (Megalin)
(Glycoprotein 330) (gp330)
Length = 4655 (1 .. 4655)

2





1

NOTE:Bitscore and expect value are calculated based on the size of the nr database.



Score = 2605 bits (6751), Expect = 0.0

Identities = 1626/4335 (37%), Positives = 2311/4335 (53%), Gaps = 270/4335 (6%)

Query	26	TCSPKQFACRDQITCISKWRCGERDCPDGSDAEPEICPQSKAQRCPNEHNCGLGTELC	85
		TC QF C CI + W CDGE DC D DE +C P E +C + C	
Sbjct	221	TCGGYQFPCPSG-RCIYQNWVCDGEDDCKDNGDEDGCGESGPHDVHKCSPREWSCPESGRC	279
Query	86	VPMSRLCNGVQDCMDGSD-----GPHCRELQNGCRLGCGHHCVPFTLDGPTCYCNSSFQ	140
		+ + ++C+G+ DC DE G +C CS L CQ+ C T G C+C +	
Sbjct	280	ISYKVCDCGILDCPREDENNTSTGKYCSMTL--CSALNCQYQCHETPYGGACFCPPGYI	337
Query	141	LQA-DGKTCCKDFDECSVYGTCSQLCTNTDGSFICGCVGYLLQPDNRSCAKNEPVDPRPP	199
		+ D +TC +FD+C ++G C Q C + G +C C EGY+L+ + CKA + +	
Sbjct	338	INHNSRSTCFEFDCCQIGICQKCESRPGRHLCHEEGYILER-GQYKANDSFGEAS-	395
Query	200	VLLIANSQNILATYLSGAQVSTITPTSTRQTTA-MDFSANETVCNVHVGSDSAAQTQLKC	258
		++ +N +++L + G + + R + F Y + V W Q ++	
Sbjct	396	-IIFSNGRDLIGDIHGRSFRILVESQNRGVAVGVAFHYHLQRFVFWT---DTVQNKVFS	450
Query	259	ARMPGLKGFVDEHTINISLSLHHEVQMAIDWL TGNFYFVDDIDDRIFVCNRRNGDTCVTLL	318
		+ GL + +N+S+ E +A+DW+ Y V+ +RI + N+G VTL+ +	
Sbjct	451	VDINGLN---IQEVLNVSVETP--ENLAVDVNNKIYLVETKVNRI DMVNLDGSRVTLI	505
Query	319	DLELYNPKGIALDPAMGKVFFTDYQGII--PKVERCDMDGQNRKTLVDSKIVFPHGITLD	375
		L +P+GIA+DP +G +FF+D+ + PK+ER MDG NR LV +K+ +P G+TLD	
Sbjct	506	TENLGHPRGIAVDPTVGYLFFSDWESLSGEPKLERAFMDGNSRKDLVKTKLGWPAGVTLD	565
Query	376	LVSRLVYWADALDYIEVDYEGKGRQTIIQG-ILIEHLYGLTVFENYLYATNSDNANAQ	434
		++S+ VYW D+ DYIE V Y+G R+T++ G LI H +G+++FE ++ T+	
Sbjct	566	MISKRVYVWDSRFDYIETVYDGIQRKTVVHGGSLIPHPFGVSLFEGQVFFTD-----W	619
Query	435	QKTSVIRVNRNFSNEYQVTVTRVD-KGGALHIYHQRQPRVRSHACENDQYKPGGCSDIC	493
		K +V++ N+F T QV + + +YH RQP + +N+ GGC +C	
Sbjct	620	TKMAVLKANKPTETNPQVYYQASLRPGYGVTVYHSLRQPYATNPCKDNN-----GGCEQVC	674
Query	494	LLA---NSHKARTCRCSGFSLGSDGKCKPEHELFLVYGKGRPGIIRGMDMGAKVPD	549
		+L+ N C+C GF L +D + C ++ FL++ IRG+ +	
Sbjct	675	VLSHRTDNDGLGFRCKCTFGFQLDTERHCIAVQN--FLIFSS--QVAIRGIPFTLTQE	730

Query	550	EHMIPNIENLMNPR---ALDFAHETGFIYFADTTSYLIGRQKIDGTERETILKDGIHNVEG	606
Sbjct	731	+ M+P+ NP +DF A+ I+F+D + ++I +QKIDGT RE + + + NVE DVMVPVSG--NPSFFVGIDPDAQDSTIFFSDMSKHMIFKQKIDGTGREILAAANRVENVES	788
Query	607	VAVDWMDNLYWTDGDPKKTISVARLEKAAQTRKTLIEGKMTHPRAIVVDPLNGWMYWT	666
Sbjct	789	+A DW+ NLYWTD K+ISV RL A +TR+T+++ + PR+ +V P G+++ +VD LAFDWISKNLYWTDHSH-YKSISVMRL--ADKTRRTTVVQ- YLNNPRSVVVHPFAGLYPFTD	844
Query	667	WEEDPKDSRRGRLERAWMDGSHRDI FVTSKTVLWPNGLSLDIPAGRLYVWDAFYDRIETI	726
Sbjct	845	W R ++ RAW DGS H + V + T+ WPNGL+ +D A RLYWVDA+ +D+IE W-----PRPAKIMRAWSDGSHL-LPVINTTLGWPNGLAIDWAASRLYVWDAYFDKIEHS	897
Query	727	LLNGTDKRKIVYEGPELNHAFGLCHHGNLFWTEYRSGSVYRLERGVGAPPTVLLRSE	786
Sbjct	898	+G DR+ + ++ H FGL G +LF+T+ +R G+ + R+ + GG +T+ +RS TFDGLDRRLRGHIEQMTHPFLGAI FGEHLFFTDWRLGAI IRVKADGGE-- -MTVIRSGI	954
Query	787	PPIFEIRMYDAQQQVGTNKRNV-- --NGGCSLCLATPG-SRQACAEQVLDAAGVTC	842
Sbjct	955	I ++ YD Q G+N C NG CS C P R C C L ++ +TC AYILHLKSYDVNIQ-TGSNACNQPTHVPGDCSHFCFPVPNFQRCVGCPIYMRASHNLTC	1013
Query	843	LANPSYVPPP-QCQGEFACANSRCIQERWKCDGNDCLDNDSEAPALCHQHTCPSDRFK	901
Sbjct	1014	+P+ PP QC F C N RC+ + CDG +DC DNDSE +TC S F EGDPTNEPTTEQCLGFSFPCKNGRCVPNYLDCDGVDDCHDNDSEQLCGTLNNTCSSAFT	1073
Query	902	CENNRKIPNRWLCDGNDNCGNSEDESNA-TCSARTCPPNQFSCASGRICI ISWTC DLD	960
Sbjct	1074	C + CIP W CD NDC + DE N T + +C Q++ + +CI W CD CD+D CGHGECIPAHWRCKDRKNDVCGSDEHNCPTHPASCLDTQYTCDNHQCISKNNVCDTND	1133
Query	961	CGDRSDSASACAYPTCFPLTQFTCNNGRCININWRCDNDNDGNDSEAGCSHSCSSQF	1020
Sbjct	1134	CGD SDE + TC P +QF C N RCI++++ CD D DC D SDE GC +C++ +QF CGDGSDEKNCNSTETCQF-SQFNCNPHRCIDLSFVCDGDKCDVDSGEVGLNCTASQF	1192
Query	1021	KCNSG-RCIEPHWTCGDNDCGDISETHANCTNQATRPFGCHCTDEFQCRDLGLCIPLR	1079
Sbjct	1193	KC SG +CI CDG DC D SDE A C TRPPG CH-DEPQC+ DG+CIPI KASGDKCIGVTNRCDGVDFCDSDNDE--AGCP-- -TRPPGMCHSDEPQCQEDGICIPNF	1247
Query	1080	WRCDGDTDCMDSDEKSCGVTHVCDPSVKFGKDSARCISKAWVCDGNDNDCEDNDS	1139
Sbjct	1248	W CDG DC+ SDE + V C PS F C D+ CI +AW+CD DNDC D SDE++ WECDGHPDCLYGSDEHNA-CVPKTC- PSSYFHC-DNGNCIHRAWLCDRDNDGCDMSDEKD	1304
Query	1140	CESLACRPPSHP---CANNTSVCLPPDKLCDGNDNDCGDSDEGELCDQCSLNNGGCSHNC	1196
Sbjct	1305	C + R PS +N V L + G + CS NGGC+H C CPTQPRCPSPWQQLGHNICVNLVSVVCDGIFDCPNGTDESPLCNGNSCSDFPNGCTHEC	1364
Query	1197	SVAPGEGIVCSPLGMLGPDNHTCQIQSYCAHLKCSQKCDQNKFSVKCSYEGVWVLEP	1256
Sbjct	1365	P G C CPLG L D+ TC+ C CSQ C + S +CSC G++LE VQEPF-GAKCLPLGLFLANDSKTCEIDECIDLGSCSQHCYNMRGSFRCSCTDGYMLES	1423
Query	1257	DGESCRSLDPKPFPIIFSNRHEIRRIDLHKGDYSV-- -LVPGLRNTIALDFHLSQSALYWT	1314
Sbjct	1424	DG + ++ ++ +++++I + + ++ LV +A+DF + +W DGRTCKVTASESLLLLVASQNKIADSVTSQVHNIYSLVENGSYIVAVDFDSISGRIFWS	1483
Query	1315	DVVEDKIYRGKLLDNGALTSFEVVIQYGLATPEGLAVDWIAGNIYVWESNLDQIEVAKLD	1374
Sbjct	1484	D + K + NG T VV + E +A+DW+ N+YW + L+ IEV+K+D DATQGTKWSA--FQNG--TDRRVVFDSSIIILTETIALDVGVRNLYWTDYALLETIEVSKID	1539
Query	1375	GTLRTTLTLAGDIEHPRAIALDPR--DGILFWTDWDASLPRIEAASMSGAGRRTVHRETGS	1432
Sbjct	1540	G+ RT L++ ++ +PR +ALDPR + +LFW+DW PRIE ASM G+ R + ++ GSHRTVLISKNLNTPRGLALDPRMEHLLFWSDWGH- PRIERASMDGSMRTVIVQDKIF	1598
Query	1433	GGWPNGLTVDYLEKRILWIDARSDAIYSARYDGSGHMEVLRGHEFLSHPFAVTLYGGVEY	1492
Sbjct	1599	WP GLT+DY + ++ +D+ D + Y+G + + + HP+A+TL+ VY --WPCGLTIDYPNRLLYFMDSYLDYMDPCDYNHGHRRQVIASDLIRHPYALTLFEDSVY	1656

Query	1493	WTDWRTNTLAKANKWTHGNVTVVQRTNTQPFDLQVYHPSRQPMAPNPCEANGGQGPCSHL	1552
Sbjct	1657	WTD T + +ANKW G N +VV P + HPS+QP + NPC + CSHL	1712
Query	1553	CLINYN--RTVSCACPHMLKHKDNTTCY-EFKKFLLYARQMEIRGVLDAPPYNYIISF	1609
Sbjct	1713	CL++ SC CP L D C + + FL+ RQ I G+ L+ +	1772
Query	1610	TVPDIDNVTVLDYDAREQVYVSDVVRTQAIKRAFINGTVGVTVVSADLPN-AHGLAVDWW	1668
Sbjct	1773	+ I N +++D EQ +YW + I R +GT S + + LA+DW+ PIAGIQGLDVEFDAAEQYIYVVE-NPGEIHRVKTDTGNTNRTVFASISMVGPSSMNLALDWI	1831
Query	1669	SRNLFWTSYDTNKKQINVARLDGSGFKNVAVQ-----GLEQPHGLVHPLRGKLYWTDGD	1722
Sbjct	1832	SRNL+ T+ T ++ D ++ ++ G+ P G+ V P RGKLYW+D SRNLYSTNPRTQSIIEVLTGLGDIRYRKTLIANDGTALGVGGFPIGITVDPARGKLYWSDQG	1891
Query	1723	N-----ISMANNMGDSNRTLLFSGQKGPVG-LAIDFPESKLYWISSGNHTINRCLNDGS	1774
Sbjct	1892	I+ ANMDG++ LF+G + + +D E KLYW +G I R N+DG+ TDSGVPKAIASNMMDGTSVTKTLFTGNLEHLECVTLDEBQKLYWATRGVIRGNVDGT	1951
Query	1775	GLEVIDAMRSQGLKATALAIMGDKLWADQVSEKMGTCADGSGSVVLRNSTTLVMHMK	1834
Sbjct	1952	++ QL +A+ L++ D+ E+ KA G+ +VLR++ + ++ DRMILV--HQLSHPWGIAVHDSFLYTYDEQYEVIERVDKATGANKIVLRDNVPLNRLGQ	2008
Query	1835	VYDESIQLDHKGTNPSCSVNNGDCSQCCLPTSETTRSCMCTAGYSLRSGQQACEGVGSFLL	1894
Sbjct	2009	VY+ + +N CS N C Q+CLP SC C G+ L ++C SF++ VYHRRNAE--SSNGCSNNMNACQQLCLPVPGLGFSACATGFKLNPDNRSCSPYNSFIV	2066
Query	1895	YSVHEGIRGIPLDPNDKSDALVPVSGTSL-AVGIDFHAENDTIYVWDMGLSTIS-----R	1948
Sbjct	2067	S+ IRG L+ +D S+ +VPV+G A+ +D + IYW D S S R VMSLSAIRGFSLELSDHSETMVPVAGQGRNALHVDVBSGGFIYWCDFSSSVASDNAIR	2126
Query	1949	AKRDQTWREDVVTNGIGR--VEGIAVDWIAAGNIYWTDOGFD--VIEVARLNGSFRVYVIS	2004
Sbjct	2127	K D + ++VT+GIG V GIAVDW+AGN+Y+T+ +EV R+N ++R V++ IKPDGSSLMNIVTHGIGENGVRGIAVDWVAGNLYFTNAFVSETLIEVLRIINTYRVRLLK	2186
Query	2005	QGLDKPRAITVHPEKGYLFWTEWGQYPIERSRLDGTERTVVLVNVSIWPNGISVDYQDG	2064
Sbjct	2187	LD PR I V P+ YLFW ++GQ P+IERS LD T R VLV+ I P G++VD DG VTVDMPRHIVVDPKPNRYLFWADYGGQRPKIERSLDCTNRTVLVSEGIIVTPRGLAVDRSDG	2246
Query	2065	KLYWCDARTDKIERIDLETGENREV-VSSNNMDMFVSFVDFEYIYWSDRTHANGSIKRG	2123
Sbjct	2247	+YW D D I R I + GEN EV+ S + ++VFB+ I W DR VYVWDDSLDIARIRIN-GENSEVIRYGSRYPTPGYITVFPNSIIWDRNLKLIKQASK	2305
Query	2124	SKDNATDSVPLRTGIGVQLDKIKVFNDRDQK-----GTNVCVAVANGGCQQLCL-YRGRG	2176
Sbjct	2306	+N +R I L+D+ +F++ Q N C NGGC LC G EPENTEPTTIVIRDNIN-WLRDVTIFDKQVQPRSPAENVNNPCLENNNGGCSHLCFALPGLH	2364
Query	2177	QRACACAHGMALEDGASCR-EYAGYLLYSERTILKSIHLSDERNLNAPVQPFEDPEHMKN	2235
Sbjct	2365	C CA G L DG +C +L+++ L+S+HL E + PF+ + TPKCDCAFGLTQSDGKNCAISTENFLIFALSNSLRLHLDPENHS----PPFQTINVERT	2420
Query	2236	VIALAFDYRAGTSGPTPNRIFFSDIHFGNIQIN---DDGSRRTITIVEN-VGSVEGLAY	2290
Sbjct	2421	V++L+D +RI+F+ + QI+ G T++ +G+ +G+A+ VMSLDYD-----SVSDRIYFTQNLASGVQGISYATLSGTHPTPTVIASGIGTADGIAF	2473
Query	2291	HRGWDTLYWTSYTTSTITRHTVDQTRPGAFAERETVITMSGDDHPRAFVLDECQNLMFWTN	2350
Sbjct	2474	D + Y + + + G+ TVI PRA VLD CQ ++W + ----DWITRRIYSDYLNQMINSMADGDS--NRTVIARV--PKPRAIVLDPCCQGYLYWAD	2525
Query	2351	WNEQPHSIMRAALSGANVLTLEIKDIRTPNGLAIDHRAEKLYFSDATLDKIERCEYDGS	2410
Sbjct	2526	W+ H I R L G + ++ + P+GL +D+ + LY+ DA+L +IER G W-DTHAKIERATLGGNFRVPIVNSSLVMPGSLTLDYEEDLLYVWDASLQRIERSTLTGVD	2584

Query	2411	RYVILKSEPHVHPFGLAVYGEHIFWTDWVRRAVQRANKHVGSNMKLLRVDIPQOPMGI-IA	2469
Sbjct	2585	R VI+ + VH FGL +Y++I+WD + + RANK+ GS + ++ QP GI REVIVNAA-VHAFGLTLYGQYIYWTDLTYQRIRYRANKYDGSQGIAMTNNLLSQPRGINTV	2643
Query	2470	VANDTNSCELSPCRINNGGCCQDLCLLTHQGHVNCSC--RGRILODDLT-CRAVNSCSCRA	2526
Sbjct	2644	V N C + PC NGGC +C G C C G L + + C N VKNQKQQCN-NPCEQFNGGCSHICAPGPNG-AECQCPHEGNWYLANNRKHCIVDNGERCG	2701
Query	2527	QDEFECANGECINFSLTCDGVPHCKDKSDEKFSYCNRRCKKTFRCQSNRCVSNMLWCN	2586
Sbjct	2702	F C+NG CI+ CD C D SDE S C C T C+NGRCV C+ ASSFTCSNGRCISEEWKCDNDNDCGDSDEMESCVALHTCSPTAFTCANGRCVQYSYRCD	2761
Query	2587	GADDCGDSDEIPCNKTACGVG-EFRCRDGTICGNSSRCNQFVDCD--ASDEMNCSATD	2643
Sbjct	2762	+DCGDSDE C C EF C + CI C N +C D SDE NC YVNDGCGDSDEAGCLFRDCNATTEFMCNNRRICPREFCNGVDNCHDNNTSDEKNCPPDR	2821
Query	2644	CSSYFRLGVKGVLPQCERTSLCYAPSWVCDGANDCGDYSDESDCPGVKRPRLPNFYAC	2703
Sbjct	2822	C S + C ++C ++CDG NDCG SDE C S + F C CQSGYT-----KCHNSNICIPRVYLCGDGNDGDSNENPTYCTTHT-CSSSEFOC	2871
Query	2704	PSGRICIPMSWTDCKEDDCHEGEDET---HCNKFCSEAQFECQNHRCISKQWLCDGSDDC	2759
Sbjct	2872	SGRCIP W CD+E DC DE H + C +F+C RCI +W+CDG +DC ASGRICIPQHWYCDQBTDCFDASDEPASCGHSERTCLADEPKCDGGRCIPSEWICDGDND	2931
Query	2760	GDGSDEAAH--CEGKTCGPSSFSFSC---PGTHVCPVERWLCDGDKDCADGADESAAGCL	2813
Sbjct	2932	GD SDE C + C S F C P C+P+ W+CDG DC DG DE+ GDMSEDEKRRHQCNQNCSDSEFLCVNDRPPDRRCIPQSWVCDGVDCTDGYDEN--QNCT	2989
Query	2814	YNSTCDDREFMCQNRQCIPKHFVCDHHRDCADGSDSESPCEYPTCGPSEFRANGRLSS	2873
Sbjct	2990	RT C + EF C CIPK F CD DC D SDE C Y TC ++F C NGRC+S -RRTCSENEFTCGYGLCIPKIFRCDRHNDGCDYSDERG-CLVQTCQNGNPTCQNGRCIS-	3046
Query	2874	RQWECDGENDCHDQSDSEAPKNPHCTSQEHKCNASSQFLCSSGRCAEALLCNQDDDCGDS	2933
Sbjct	3047	+ + CD +NDC D SDE C + E C +F C +GRC+ LCN DDC D+ KTFVCEDENDGCGDSDELMHL--CHTPEPTC-PPHEFKCDNGRCIEMMKLCNHLDDCLDN	3103
Query	2934	SDERGCHINECLSRKLSGCSQDCEDLKIGFKRCRPGFRLKDDGRTCADVDECSTT-FPC	2992
Sbjct	3104	SDE+GC INEC +SGC +C D F C CRPG++L D RTC D+DEC+ F C SDEKGCINECHDPSISGCDHNCTDTLTSFYCSCRPGYKLMSDKRCTVDIDECTEMPFC	3163
Query	2993	SQRCINTHGSYKLCVVEGYAPRGDPHSCKAVTDEEPLIFANRYLRKLNLDGSNYTLL	3052
Sbjct	3164	SQ+C N GSY C C GY R D +C+ ++EP+LIF+NRYYLR L +DG Y+L+ SQKCEVNIYSYICKCAPGYL-REPDGKTCRQNSNIEPYLIFSNRYLRNLTIDGYFYSLI	3222
Query	3053	KQGLNNAVALDFDYREQMIYWDVTQTQGSIMRMHLNGSNVQVLHRTGLSNPDGLAVDWV	3112
Sbjct	3223	+GL+N VALDFD E+ +YW D TQ +I RM LN +N + + L + LAVDWV LEGLDNVVALDFDRVEKRLYWD--TQRQVIERMFLNKTNETIINHRLPAESLAVDWV	3280
Query	3113	GGNLYWCDKGRDTEIEVSKLNGAYRTVLVSSGLR-----EPRALVVDVQNGYLYWTDW	3164
Sbjct	3281	LYW D + VS LNG +R +L + PR L + G GYLYW DW SRKLYWLDARLDGLFVSDLNGGHRMLAQHCVDANNTFCFDNPRGLALHPQYGYLYWADW	3340
Query	3165	GDHSLIGRIGMDGSSRSVVDTKITWPNGLTLDYVTERIYADAREDIYEFASLDGNSRH	3224
Sbjct	3341	G + IGR+GMDG+++SVI+ TK+ WPNG+T+DY + +YADA YIE++ L+G +RH GHRAYIGRVGMDGTNKSVIISTKLEWPNGITIDYTDNLLYWAHAHGYIEYSDLEGGHHR	3400
Query	3225	VVLSQDIPHIFALTLFEDYVYWDWETKSNINRAHKTGTGINKTLLISTLHRPMDLHVPHAL	3284
Sbjct	3401	V +PH FA+T+T+P+YWDW T+++ + +K G+N+ L++T HRP D+HV+H TVYDGAIPHPPAIFTBDDTYWTDWNTRTVEKGNKYDGSNRQTLVNTTHRPDIHVHPY	3460
Query	3285	RQPDVNPVHPCVNNNGGCSNLCLLSPGG-GHKACAPTNF-YLGSDEGRT-CVSNCTASQFVC	3341
Sbjct	3461	RQP V N PC NNGGCS+LCL+ PGG G C CP +F G L T C +C+++QF+C RQPIVSN-PCGTNNNGGCSHLCLIKPGKGFTCECPDDFRTLQSGSTYCMPCMSSTQFLC	3519

Query	3342	-KNDKCIPIFWKCDTEDDCGDHSDPEPDDCPEFKCRPGQFCSTGICTNPAPICDGDNDQ	3400
		N+KCIPI WKKCD + DC D SDE CP+ CR GQFQCS G CT+P +C+ +C	
Sbjct	3520	ANNEKCIPIWKKCDGQKDCSDGDELALCPQRFCLRGQFQCSGDNCTSPQTLCAHQNC	3579
Query	3401	DNSDEAN--CDIHVCLSPQFKCTNTNRCIPGIFRCNQDNCGDG--EDERDCPEVTCA	3456
		D SDE C+ H C ++++C N RCIP ++++C D ED C TC P	
Sbjct	3580	DGSDERDLLENHCHDSNEWQCAN-KRCIPESWQCDTFDNCEDNSDESSHASRTPCR	3638
Query	3457	QFQCSITKRCIPRVVWVCDRNDNCDVGSDEP----ANCTQMTGCVDEFCKDNGRCIPAR	3512
		WQF+C+ RCIP+ W CD DNDC D SDEP + + EF CK + RCIP +W	
Sbjct	3639	QPRCA-NGRCIPQAWKCDVDNDCGDHSDPEIEECMSAHLCDNFTEFSCKTNYRCIP-K	3696
Query	3513	KCDGEDDCDGDSDPEKCECDERTCEPY-QFRCKNNRCVPGRWQCDYDNDCGDNDSEES	3571
		CT + ++ C+ERTC P FRCKN+ C+P RWQCD NDCGDNDSDEE+C	
Sbjct	3697	-AVCNGVDDCRDNDSDGQCEERTCHPVGDFRCKNHHCIPLRWQCDGQDNDCGDNDSE	3755
Query	3572	PRPCESEFEFCANGRCIAGRWKCDGDHDCADGSDSEKCDKTPR-CDMDQFQCKSGH	3630
		CIPLRW PR C+ESEF C N +CI RW CD +DC D SDE+DC R C + FQC SGHC+	
Sbjct	3756	PRECTESEFRVCNQCIPSRWICDHYNDCGDNDSEDERDCMERTCHPEYFQCTSGHCV	3815
Query	3631	RCADADACMDGSDDEEACGTGV---RTCPLDEFQCNNTLCKPLAWKCDGEDDCGDN	3687
		SDENP +CD ADC+D SDE C T C F+C N +C P WKCDG+DDCGD SDE	
Sbjct	3816	KCDGSADCLDASDEADCPTRFPDGAQCQATMFECKNHVCIIPPYWKCDGDDDCGDS	3875
Query	3688	EECARFVCPNPRPFRCNKDRVCLWIGRQCDGTDNCGDGTDEEDCEPPTAHTTHCKDK	3747
		KEF C C FRC N+R C++ C+G D+CGDGTDE + C+ E+	
Sbjct	3876	HLCLDVPFCNSPNRPFRCNNR-CIYSEHVCNGVDDCGDGTDETEEHCRKPTKPKTE	3933
Query	3748	LRCNRQCLSSSLRCNMFDDCGDGSDEEDCSIDPKLTSCATNASICGDEARCVRTEKA	3806
		AY-C N G+ C+ DDCGD SDE C+ K +CA N IC E C+ + +	
Sbjct	3934	KCGNGHCIPHDNVDCDADDGSDDELGCN-KGKERCTAEN--IC--EQNCTQLNVEG	3988
Query	3807	CACRSGFHT-VPGQPGQDINECLRFGTCSQLCNNTKGGHLCSARNFM---KTHNTCK	3861
		C+C +GF T V + C DINEC +FGTC Q C NTKG + C CA F + C	
Sbjct	3989	CSCTAGFETNVFDRTSCLDINECEQFGTCQHCNRTKGSYECVADGFTSMSTRPGK	4048
Query	3862	AEGSEYQVLYIADNEIRSL-FPGHPHSAIEQAQFGDESVRIDAMDVHVKAAGRVYTN	3920
		WNH AEGS +L + D+ IR S Y Q + ++V D + VY+T	
Sbjct	4049	AEGSS-PLLLLDPNVIRKYNLSSERFSEYLQDEEYIQAVDYDWDPKDIGLSVVYYT	4107
Query	3921	TGTISYRSLPPAAPPTTSNRHRRQIDRGVTHLNLISGLMKPRGIAIDWVAGNVYWT	3980
		SDGRD G+ + + A P + + L + + P GIA+DWV ++Y+D	
Sbjct	4108	EGS-RFGAKRAYIPNFESGRNNLVQE--VDLKLKYVMQPDGIAVDWVGRHYWSDV	4164
Query	3981	VIEVAQMKGENRKTLSGMDPEHAIVVDPLRGTMYSWDGWNHPKIETAAMDGTLR	4040
		ETLV IEVA++ G RK LIS +D+P AI V+P G M+W+DWG PKIE+A M+G R LV	
Sbjct	4165	RIEVAKLDRGRYKWLISDTLDQPAIAVNPGLGMFWTDWGKEPKIESAWMNGEDR	4224
Query	4041	QDNIQWPTGLAVDY-HNERLYWADAKLSVIGSIRLNGTDPIVAADSKRGLSHPF	4099
		SIDVFE +++ WPTGL++DY +N+R+YWD K VI +I+ +GTD V A + +P+S+D+FE	
Sbjct	4225	FEDLGWPTGLSIDYLNNDRIYWSDFKEDVIETIKYDGTDRRVIA---KEAMPYSL	4281
Query	4100	DYIYGVTYINNRFVKIHKFGHSPVLNLTGGLSHASDVVLYHQHK-QPEVTNPCR	4158
		KKCEW D+Y ++ V+K +KFG + V ++HQ + V N C + + C	
Sbjct	4282	DQLYWISKEGEVWQKFKFGQKKEKTLVNPWLTVRIFHQLRYNKSVPNLNC-KQICS	4340
Query	4159	LCLLSPSGPVCTCPNGKRLDNGTCVPVPSPTPPDAPRPGTCNLQCFNGGSCFLN	4218
		NARRQP LCLL P G C CP G G+ + P P +C +GG+C+ + P	
Sbjct	4341	LCLLRPGGYSCACPGGSSFIEGSTTECDAAIELPINLPP---PCRCMHGNCYFDE	4397
Query	4219	KCRCQPRYTGDKCEL 4233	
		KC+C YTG CE+	
Sbjct	4398	KCKCPSGYTGKYCEM 4412	



Score = 595 bits (1535), Expect = 4e-167

Identities = 372/1068 (34%), Positives = 536/1068 (50%), Gaps = 88/1068 (8%)

```

Query 840 VTCLANSPYVPPQCPQGEFACANSRCIQERWKCDGDNDCLDNSDEAPALCHQHTCPSDR 899
      V CLA S +C F C + CI W+CDG DC D+DE C TC
Sbjct 17 VACLAPAS---GQECDSAHRFCGSGHCIPADWRCDGTKDCSDDADEIG--CAVVTCCQGY 71

Query 900 FKCENN-RCIPNRWLCDGDNDCGNSEDESATCSARTCPPNQFSCASGRICIPSWTCDL 958
      FKC++ +CIPN W+CD D DC + DE CS TC +Q+C++G+CIP + CD
Sbjct 72 FKCQSGQCIPIPSWVCDQDQDCDDGSDERQ-DCSQSTCSSHQICSPNQCIPEYRCDHV 130

Query 959 DDCGDRSDESACAYPTCFPLTQFTCNNGRCININWRCDNDNDCGNSDEAGCSHSCSST 1018
      DC D +DE+ C YPTC Q TC+NG C N + +CD DC D+SDE C+ C
Sbjct 131 RDCPDGADEN-DCQYPTC---EQLTCNAGACYNTSQKCDKWVDCRDSDEINCTEICLHN 186

Query 1019 QFKCNSGRCIPEHWTCDDGNDGCDYSDETHANCTNQTARPPGGCHTDEFQCRDLGLCIPL 1078
      +F C +G CIP + CD DNDC D SDE N C +F C G CI
Sbjct 187 EFSCNGNECIPRAYVCDHDNDGQDGSDEHACNYPT-----CGGYQFTCP-SGRCIYQ 237

Query 1079 RWRCDGDTDCMDSDEKSCRG---VTHVCDPSVFGCKDSARCISKAWVCDGNDNDCEDNS 1135
      W CDG+ DC D+ DE CE H C P ++ C +S RCIS VCDG
Sbjct 238 NWVCDGEDDDGNDGDEGCGESGPHDVHKCSPR-EWSCPESGRGISIYKVCDEG----- 288

Query 1136 DEENCESLACRPPSHPCANNTSVCLPPDKLCDGNDDCGDSDEGELCDQCSLNNGGCSHN 1195
      L C P NNTS + CS N C +
Sbjct 289 -----ILDC--PGREDENNTST-----GKYCSMTLCSALN--CQYQ 320

Query 1196 CSVAPGEGIVGCSCPLGMELG-PDNHTCQIQSYCAKHLKCSQKCDQNKFSVKSCSYEGWVL 1254
      C P G C CP G + D+ TC C C QKC+ C C EG++L
Sbjct 321 CHETPYGG-ACFCPPGYIINHNSRTCEVFDDCQIWGICQDKCESRGRHLCHCEGYIL 379

Query 1255 EPDGESCRSLDPF-KPFIIFS NRHEIRRIDLHKGDYSVLVPLRLNTIALD--FHLQSAL 1311
      E G+ C++ D F+ IIFSN ++ D+H + +LV +A+ FH +
Sbjct 380 E-RGQYCKANDSFGEASIIFSNGRDLIGDIHGRSFRILVESQNRGVAVGVAFYHLQRV 438

Query 1312 YWTDVVEDKIYRGKLLDNGALTSFEVVIQYGLATPEGLAVDNIAGNIYWVESNLQIEVA 1371
      +WTD V++K++ + NG + + V+ + TPE LAVDN+ IY VE+ ++I++
Sbjct 439 FWTDTVQNKVFSVDI--NG--LNIQEVLVSVETPENLAVDVVNKNKLYLVETKVNRI DMV 494

Query 1372 KLDGTLRTLLAGDIEHPRAIALDPRDGILFWTDWD--ASLPRIEAASMSGAGRRTVHRE 1429
      LDG+ R TL+ ++ HPR IA+DP G LF++DW+ + P++E A M G+ R+ + +
Sbjct 495 NLDGSYRVLITENLGHPRGIAVDPTVGYLFFSDWESLSGPEKLERAFMDGNSNRKDLVKT 554

Query 1430 TSGSGWPNGLTVDYLEKRIWIDARSDAIYSARYDGSGHMEVLRGHEFLSHPPFVATLYGG 1489
      GWP G+T+D + KR+ W+D+R D I + YDG V+ G + HPF V+L+ G
Sbjct 555 --KLGPAGVTLDMISKRVYVWDSRFDYIETVYTDGIQRKTIVVHGGSLIHPFVGSLEFEG 612

Query 1490 EYVWTDWRTNTLAKANKWTGHNVTVVQRTNTQPFDLQVYHPSRQPMAPNPCEANGQGQPC 1549
      +V++TDW + KANK+T N V + + +P+ + VYH RQP A NPC+ N G C
Sbjct 613 QVFTPDWTKMAVLKANKFTETNPQVYQASLRPYGVTVVHSLRQPYATNPCKDN--NGGC 670

Query 1550 SHLCLINYNRT-----VSCACPHMLKHLKNDNTTCYEFKFLLYARQMEIRGVLDLAPYYN 1604
      +C++++ C C +L D C + FL+++ Q+ IRG+
Sbjct 671 EQVCVLSHRTDNDGLGRCKCTFGQLDTRERHCIAVQNFLIFSSQVAIRGIPFTLSTQE 730

Query 1605 YIISFTVPIDINVTVLDYDAREQRYVWSVVRTQAIKRAFINGTGVETVVSADLPNAHGLA 1664
      ++ + +D+DA++ ++SD+ I + I+GTG E + + + N LA

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Sbjct 731 DVMVPVSGNPSFFVIGIDFDAQDSTIFFSDMSKHMIFKQKIDGTGREILAAANRVENVESLA 790

Query 1665 VDWVSRNLFWTSYDTNKKQINVARLDGSGFNNAVVGLEQPHGLVHVHPLRGKLYWTD---G 1721
DW+S+NL+WT D++ K I+V RL + VVQ L P +VVHP G L++TD
Sbjct 791 FDWTSKNLYWT--DSHYKSISVMRLADKTRRTVVQYLNPNRPSVVVHPFAGYLFFTDWRFP 848

Query 1722 DNISMAMNMGDSNRTLLFSGQKG-PVGLAIDFPESKLYWISSGNHTINRCNLDGSGLEVID 1780
I A DGS+ + + G P GLAID+ S+LYW+ + I DG +
Sbjct 849 AKIMRAWSDGSHLLPVINTTLGWENGLAIDWAASRLYWDAYFDKIEHSTFDGLDRRLRG 908

Query 1781 AMRSQLGKATALAIMGDKLWADQVSEKMGTCCKADGSGSVVLNRNSTLVMHMKVYDESI 1840
+ Q+ LAI G+ L++ D + KADG V+R+ ++H+K YD +I
Sbjct 909 HI-EQMTHPPLGALIFGEHLFFTDWRLGAIIRVRKADGGEMTVIRSGIAYILHLKSYDVNI 967

Query 1841 QLDHKGNTNPCSVNNGDCSQLCLPTSETTRSCMCTAGYSLRSGQOACEG 1888
Q N + NGDCS C P R C C G L S CEG
Sbjct 968 QTGSNACNQPTHPNGDCSHFCPPVPNFQVRVCGCPYGMRLASNHLTCEG 1015

```



Score = 428 bits (1100), Expect = 1e-116
 Identities = 261/716 (36%), Positives = 367/716 (51%), Gaps = 56/716 (7%)

```

Query 2640 SATDC-SSYFRLGVKGLVFPQCERTSLCYAPSWVCDGANDCGDYSDERDCPVPRCPL 2698
+ C S++FR G + C W CDG DC D+DE C V C
Sbjct 24 SQQECSAHPFRG-----SGHCIPADWRCDGTKDCSDDADEIGCAVVT--CQQ 69

Query 2699 NYFACPS-GRCIPMSWTCDEKEDCEHGEDETH-CNKF-CSEAQFECQNHRCISKQWLCDG 2755
YF C S+CIP SW CD++ DC+ G DE C++ CS Q C N+CI ++ CD
Sbjct 70 GYFCKSQEQGQCIPNSWVCDQDQDCDGDSDERQDCSQSTCSSHQITCSNGQCIPSEYRCDH 129

Query 2756 SDDCGDGSDEAAHCEGKTCGPSSFCPGTHVCVPERWLCDGDKCADGADEIAAGCLYN 2815
DC DG+DE C+ TC +C + + + CL+N
Sbjct 130 VRDCPDGADEN-DCQYPTC--EQLTCDNGACYNTSKQCDKWKVDCRDSSDEINCTEICLHN 186

Query 2816 STCDDREFMCONRQCIPKHFVCDHHRDCADGSDSEPECEYPTCGPSEFRANCGRCLSSRO 2875
EF C N +CIP+ +VCDHD DC DGSDE C YPTCG +F C +GRC+ +
Sbjct 187 -----EFSCGNGECIPRAYVCDHNDQCQDGSDEHA-CNYPTCGGYOFTCPSGRCIY-QN 238

Query 2876 WECDEGENDCHDQSD--APKNPHCTSQEHKCNASSQFLCSSGRCAEALLCNQDDCGDS 2933
W CDGE+DC D DE PH HKC+ SGRC++ +C+G DC
Sbjct 239 WVCDGEDDCKDNGDEGCEGPH--DVHKCSPREWSCPESGRCSISYKVCDDGILDCPGR 295

Query 2934 SDERGCHINECLSRKLSG--CSQDCEDLKIGFKRCRCRPGFLK-DDGRTCADVDECSST 2989
DE + S L C C + G C PG+ +D RTC +D+C
Sbjct 296 EDENNTSTGKYCSMTLCSALNCQYQCHETPYGGACFCPPGYIINHNSRTECVFEDDCQIW 355

Query 2990 FPCSQRICINTHYSKYLCEVGYAPRGDPHSCKAVID-BEPFLIFANRYLRKLNLGDSN 3048
C Q+C + G + C C EGY G CKA E +IP+N L L++G
Sbjct 356 GICDQKCESRPGRHLCHEEGYILERGQ--YCKANDSFGEASIIFSGNRDLIGDIHGRS 413

Query 3049 YTLKQKGLNNAVALD--FDYREQMIYWTDVTTQGSIMRRMLNGSNVQVLHRTGLSNPDG 3106
+ +L + N VA+ F Y Q ++WTD T + + + +NG N+Q + + P+
Sbjct 414 FRILVDSQNRGVAVGAFYHLQRVFTD--TVQNKVFSVDINGLNIQEVNLNVSVETPEN 471

Query 3107 LAVDWVGGNLYLCKDKGRDTEVSKLNGAYRTVLVSSGLREPRALVVDVQNGYLYWTDWGD 3166
LAVDWV +Y + + I++ L+G+YR L++ L PR + VD GYL++WDW
Sbjct 472 LAVDWNNKILYLVETKVNRIDMVNLDGSYRVTLITENLGHPRGIADVPTVGYLFFSDWES 531

Query 3167 HS---LIGRIGMDGSSRSVIVDTKLTWPNGLTLDYVTERIYWADAREDYIEFASLDGSNR 3223

```



```

      S   + R MDGS+R +V TK+ WP G+TLD +R+Y+D+R DYIE + DG R
Sbjct 532  LSGEPKLERAFMDGSGNRKDLVTKLGWPAGVTLDMISKRVYVWDSRFDYIETVYDGIQR 591

Query 3224  HVVL--SQDIPHIFALTLFEDYVYVTDWETKSIINRAHKTGTGNTKLLISTLHRPMDLHV 3281
      V+   IPH F ++LFE V++TDW ++ +A+K T TN +   RP + V+
Sbjct 592  KTVVHGGSLLIPHPFGVSLFEGQVFFTDWTKMAVLKANKFTETNPQVYQASLRYPGVTVY 651

Query 3282  HALRQPDVPHNPKCVKNNGGCSNLCLLS-----PGGSHKACPTNFYLGSDGRTCVS 3332
      H+LRQP N PCK NNGGC +C+LS G G +C C F L +D R C++
Sbjct 652  HSLRQPYATN-PCKDNNGGCEQVCVLSHRTDNDGLGRCKCTFGPQLDTERHCIA 706

```



Score = 376 bits (966), Expect = 4e-101

Identities = 267/841 (31%), Positives = 407/841 (48%), Gaps = 58/841 (6%)

```

Query 24    PKTCSKPQFACRDQITCISKGWRCDDGERDCPDGSDAEIPCQSAQRCQPNNEHNCGLTE 83
      PKTC F C D CI + W CD + DC D SDE CP ++ + RC + CLG
Sbjct 1268  PKTCPSSYFHC-DNGNCIHRALWCDRDNDCGDMSDEKD--CP-TQPFRCPSQWQCLGHN 1323

Query 84    LCVPM SRLNCNVQDCMDGSDGPHCRELQGNCSRLGCGQHHCVPTLDGPTCYCNSSPOLQA 143
      +CV +S +C+G+ DC +G+DE P C + GC H CV G C C F L
Sbjct 1324  ICVNLSCVCGDIFDCPNGTDESPLCNNGSCSDFNGGCTGCEQEFPGAKCLPLGFLAN 1383

Query 144   DGKTKCDFDECSVYGTCSQLCTNTDGSFICGCVGYLLQPDNRSCAKNEPVD RPPVLLI 203
      D KTC+D DEC + G+CSQ C N GSF C C GY+L+ D R+CK +LL+
Sbjct 1384  DSKTCEDIDECDILGSCSQHCYNMRGSPRCSCTDGYMLES DGRCTCKV--TASESLLLLV 1440

Query 204   ANSQNILA-TYLSGAQVSTITPTSTRTQTAMDFSYANETVCVWVHVGSDAAQTOLKCARMP 262
      A+ I+A + S + A+DF + + W A Q + A
Sbjct 1441  ASQNKIIADSVTSQVHNIYSLVENGSIYIVAVDFDISGRIFW----SDATQGTKWSAFQN 1496

Query 263   GLKGFVDEHTINISLSLHHVEQMAIDWLTGNFYFVDDIDDRIFVCNRNGDTCVTLDDLLEL 322
      G + + S+ E +AIDW+ N Y+D + I V +G L+ L
Sbjct 1497  G----TDRRVVDFSSIIILTETIADWVGRNLYWTDYALETIEVSKIDGSHRTVLISKNL 1551

Query 323   YNPKGIALDPAMKG--VFETDYGQIPKVERCDMDGQNRKLVDSKIVFPHGITLDLVSR 380
      NP+G+ALDP M + +F++D+G P++ER MDG RT +V KI +P G+T+D +RL
Sbjct 1552  TNPRGLALDPFRNHEHLLFWSDWGHHPRIERASMDGSMRTVIVQDKIFWPGLTIDYPNRL 1611

Query 381   VYWADAYLDYIEVVDYEG-KGRQTI IQGLIEHLYGLTVFENYIATNSDANAQAQKTS 439
      +Y+ D+YLDY++ DY G RQ I ++I H Y LT+FE+ +Y T D A + V
Sbjct 1612  LYFMDSYLDYMDFCYNGHRRQVIASDLIIRHPYALTLFEDSVYWT--DRATR----V 1665

Query 440   IRVNRNFNSTEYQVVT-RVDKGGALHIYHQRQPRVRSHACENDQYKPGGSCIDCLLAN- 497
      +R N+++ VV + + H +QP + C + CS +CLL++
Sbjct 1666  MRANKWHGNGQSVVMYNIQWPLGIVAVHPSKQPN-SVNPCAFSR-----CSHLCLLSSQ 1718

Query 498   SHKARTCRCSRGSFSGSDGKSCCKPEHELFLVYKGGRGPIIRGMDMGAKV-PDEHMIPIE 556
      +C C SG+SL D +C + + + R II G+ + +V ++ M+PI
Sbjct 1719  GPHFYSCVCPGWSLSPDLLNCLRDDQPFLITV---RQHIIFGSLNPEVKNSDAMVPIA 1775

Query 557   NLNMPRALDFHAETGFIYFADTTSYLIGRQKIDGTERETILKDGINHVE-GVAVDWMGDN 615
      + N ++F +IY+ + I R K DGT R + + +A+DW+
Sbjct 1776  GIOQLDVEFDDAEQYIYWVENPGE-IHRVKT DGTNRTVFASISMVGPMSNMLALDWISRN 1834

Query 616   LYWTDGDPKKTISVARLEKAAQTRKTLIEGKMT-----HPRAIVVDPLNGWMYWTDWEED 670
      LY T+ ++I V L + R KTLI T P I VDP G +Y+D D
Sbjct 1835  LYSTNP-RTQSIEVLT LHGDIYRKTLIANDGTALGVGFPPIGITVDPARGKLYWSDQGTD 1893

```

```

Query 671 PKDSRRGRRLERAWMDG--SHRDIFVTSKTVLWPNGLSLDIPAGRLYVWDAFYDRIETILLN 729
      ++ A MDG S ++ F + L ++LDI ++LYW IE ++
Sbjct 1894 --SGVPKAIASANMDGTSVKTLFTGNLEHL--ECVTLDIEEQKLYWAVTGRGVIERGNVD 1949

Query 730 GTDRKIVYEGPELNHAFGLCHHGNYLFWTEYRSGSVYRLERGVGGAPPTVTLRSERPPI 789
      GTDR I+ ++L+H +G+ H ++L++T+ + + R+++ G ++LR P +
Sbjct 1950 GTDRMILVH--QLSHPWGIAVHDSFLYYTDEQYEVIERVDKATGA---NKIVLRDNPVNL 2004

Query 790 FEIRMYDAQQQQVGTNKRNVNNGCCSSCLATPGSR--QCACAEDQVLADGVTCLANPSY 848
      +++Y + + +N C N C +CL PG CACA L+ D + C S+
Sbjct 2005 RGLQVYHRRNAAESSNGCSNMNMACQQICLPVPGGLFSCACATGFKLNPDRSCSPYNSF 2064

Query 849 V 849
      +
Sbjct 2065 I 2065

```

Score = 320 bits (819), Expect = 4e-84

Identities = 219/745 (29%), Positives = 324/745 (43%), Gaps = 93/745 (12%)

```

Query 3453 CAPNQFQCSITKRCIPRVWVCDRDNDGSDSEFANCTQMTGCVDEFCKDNGSRICIPARW 3512
      C F+C + CIP W CD DC D +DE C +TC F+C + G+CIP +
Sbjct 28 CDSAHFRCG--SGHCIPADWRCGTGKDCSDDADE--IGCAVVTQQQYFKCQSEGOQIPNSW 85

Query 3513 KCDGEDDCGSDGSEPKKECEDERTCEPYQFRCKNNRCPVGRWQCDYDNDCGDNDSEESCTP 3572
      +D D + +++C + TC +Q C N +C+P ++CD+ DC D +DE C
Sbjct 86 -VCDQDQDCDDGSDERQDCSQTCSHQITCSNGQICPSEYRCDHVRDCPDGADENDCQY 144

Query 3573 RPCSESEFSCANGRCIAGRWKCDGDHDCADGSDDEKDCDTPRCMDQFQCKSGHCIPLRWRC 3632
      C + +C NG C KCD DC D SDE +CT C ++F C +G CIP + C
Sbjct 145 PTCEQ--LTCDNAGACYNTSQKCDWKVDCRDSSEINCTEICLHNFEFCGNGECIPRAVVC 202

Query 3633 DADADCMGSDSEECAGTGVTRCPLDEFQCNNTLCKPLAWKCDGEDDCGDNNDENPEECAR 3692
      D D DC DGSDE AC TC +F C + C W CDGEDDC DN DE+ E
Sbjct 203 DHDNDQDQSDGSEHACN--YPTCGGYQFTCPSGRCIYQNVVWCDGEDDCCKNGDEDCGSE- 259

Query 3693 FVCPPNRPFRCKNDRVCLWIGRCQDGTDCGDTDEEDCEPTAHTTHCKDKKEFLC-RN 3751
      H H ++E+ C +
Sbjct 260 -----PHDVHKCSPREWSCPE 276

Query 3752 QRCLSSSLRCNMFDDCGDSDDEEDCSIDPKLTSCATNASICGDEARCVRTEKAAYCACRS 3811
      RC+S C+ DC DE + S + +A C + +C T C C
Sbjct 277 GRCISIIYKCDGILDCPGREDENNNTSGKYCSMTLCSALNC--QYQCHETPYGGACFCPP 334

Query 3812 GFHTVPQGPQ--QDINECLRFGTCSQLCNNTKGGHLCSCARNF--MKTHNTCKAEGSEYQV 3869
      G+ C + ++C +G C Q C + G HLC C + ++ CKA S +
Sbjct 335 GYIINHNDNRCTCFEFDCCQIWIGICDQKCESRPGRHLCHEBGYILERGQYCKANDSPGEA 394

Query 3870 LYIADNNEIRSLFPGPHPS--AYEQAFQGDSEVRIDAMDVHVKAGRVYTNWHTGTISYRS 3928
      I + R L G H ++ + + H RV+WT+
Sbjct 395 SIIFSNG--RDLIGDIGHRSFRILVESQNRGVAVGAFHYHLQRFVPTD----- 442

Query 3929 LPPAAPPTTSNRHRRQIDRGVT--HLNISGLKMPRGIAIDWVAGNVYWTDSGRDVEVA 3985
      T N+ G+ LN+S ++ P +A+DWV +Y ++ + I++
Sbjct 443 -----TVQNKVFSVDINGLNIQVFLNVS--VETPENLAVDVNNKILYVETKVNRI DMV 494

Query 3986 QMKGENRKTLSIGMIDEPHAIIVDPLRGTMYSWSDW---GNHPKIETAAMDGTLRRETLVQD 4042
      + G R TLI+ + P I VDP G +++SDW PK+E A MDG+ R+ LV+
Sbjct 495 NLDGYSYRVTLITENLGHPRGIAVDPTVGYLFFSDWESLSGEBPKLERAFMDGSNRKDLVKT 554

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```

Query 4043 NIQWPTGLVADYHNERLYWADAKLSVIGSIRLNGTDPIVAADSKRGLSHPPSIDVFEDIY 4102
          + WP G+ +D ++R+YW D++ I ++ +G + HPF + +FE +
Sbjct 555 KLGWPAGVTLDMISKRVYVWDSRFDIETVTVYDGIQRKTVVHGGLIPHPFGVSLFEGQV 614

Query 4103 YGVTYINNRFVKIHKFGH-SPLVNLTGGLSHASDVVLYHQHQPEVTNTPC--DRKKCEWL 4159
          + + V K +KF +P V L V +YH +OP TNPC + CE +
Sbjct 615 FPTDWTMKAVALKANKFTETNPQVYQASL-RPYGVTVYHSLRQPYATNPCKDNNGGCEQV 673

Query 4160 CLLSPS-----GPVCTCPNGKRLD 4178
          C+LS G C C G +LD
Sbjct 674 CVLSHRTDNDGLGFRCKCTFGFQLD 698

```



Score = 263 bits (671), Expect = 6e-67
 Identities = 166/497 (33%), Positives = 253/497 (50%), Gaps = 40/497 (8%)

```

Query 25 KTCSPKQFACRDQITCISKWRCDEGRDCPDGSDEAPEICPOSKAQRCPQNEHNCIGTEL 84
          +TC QF C++ CISK + CD + DC DGSDE +C + C P+E C
Sbjct 3030 QTCQOQOFTCQNG-RCISKFTVCEDENDNCDGSDSDELMHLC-HTPEPTCPHPEFKC-DNGR 3086

Query 85 CVPMSRLCNGVQDCMDGSDSE-GPHCRELQGNCSRLGCGHHCVPITLDGPTCYCNSSFQLQA 143
          C+ M +LCN + DC+D SDE G E + S GC H+C TL C C ++L +
Sbjct 3087 CIEMKMLCNHLDDCLDNDSEKGCGINECH-DPSISGCDHNCTDLTSTFYCSCRPGYKMLS 3145

Query 144 DGKTKCDFDECSVYG-TCSQLCTNTDGSFICGCVGYLLQPDNRSCAKNEPVDPRPVL 202
          D +TC D DEC+ CSQ C N GS+IC C GYL +PD ++C +N ++ P L+
Sbjct 3146 DKRTCVDIDECTEMPFVCSQKCENVIGSYICKCAPGYLREPDPGKTCR-QNSNIE--PYLI 3202

Query 203 IANSQNILATYLSGAQVSTITPTSTROTMTAMDFSANETVCVWHVGDSSAAQTOLKCARMP 262
          +N + + + G S I A+DF + + W+ TQ +
Sbjct 3203 FSNRYRLNRLTIDGYFYSLILEGLDNV-ALDFRVEKRLYWI-----DTQRQVIERM 3254

Query 263 GLKGFVDEHTINISLSLHVEQMAIDWLGTGNFYFVDDIDDRIFVCNRRG-----DTCV 315
          L E IN L E +A+DW++ Y++D D +FV + NG CV
Sbjct 3255 FLNKTNKETIINHRLPA--AESLAVDWVSRLYLWDLARLDGLFVSDLNGHRRMLAQHCV 3312

Query 316 TLLDLELY-NPKGIALDPAMGKVFFTDYQGQIPKVERCDMDGQNRKLVDSKIVFPHGITL 374
          + + NP+G+AL P G +++ D+G + R MDG N++ ++ +K+ +P+GIT+
Sbjct 3313 DANNTFCFDNPRGLALHPQGYLYWADWGHGRAYIGRVGMDGTNKSVIIISTKLEWPNGITI 3372

Query 375 DLVSRVLVWADAYLDYIEVDYEGKGROTIIOGILIEHLYGLTFPENLYATNSDNANAQ 434
          D + L+YWADA+L YIE D EG R T+ G L H + +T+FE+ +Y T+ +
Sbjct 3373 DYTNDLLYWADAHLGYIEYSDLEGHHRHTVYDGDAL-PHPFAITIFEDTIYWTDWNT--- 3427

Query 435 OKTSVIRVNRNFNSTEYQ-VVTRVDKGGALHIYHORRQPRVRSHACENDQYKPGGCSDIC 493
          +V + N+++ + Q +V + +H+YH ROP V + N+ GGCS +C
Sbjct 3428 --RTVEKGNKYDGSNRQTLVNTTHRPFDIHVYHPYRQPIVSNPCGTNN-----GGCSHLC 3480

Query 494 LLANSHKARTCRCSRGF 510
          L+ K TC C F
Sbjct 3481 LIKPGGKGFTCECPDDF 3497

```



Score = 220 bits (561), Expect = 3e-54

Identities = 113/286 (39%), Positives = 148/286 (51%), Gaps = 12/286 (4%)

```

Query 3413 CLPSQFKCTNTNRCIPGIFRCNGQDNCGDGEDERDCPEVTCAPNQFQCSITKRCIPRVWV 3472
           C + F+C + CIP +RC+G +C D DE C VTC F+C +CIP WV
Sbjct 28 CDSAHFRC-GSGHCIPADWRCDGTkDCSDDADEIGCAVVTCCQQGYFKCQSEGCIPNSWV 86

Query 3473 CDRDNCVDGSDSEPANCTQMTGCVDEFRCKDSGRICIPARWKCDGEDDCGSDGSEPKKEECD 3532
           CD+D DC DGSDE +C+Q TC + C +G+CIP+ ++ + +C
Sbjct 87 CDQDQCDGSDSDEKQDCSQSTCSSHQITC-SNGQCIPSEYR--CDHVRDCPDGADENDCQ 143

Query 3533 ERTCEPYQFRCKNNRCVPGRWQCDYDNDCGDNSDEESCTPRPCESEFSCANGRCIAGRW 3592
           TCE Q C N C +CD+ DC D+SDE+CT C +EFSC NG CI +
Sbjct 144 YPTCE--QLTCDNGACYNTSQKCDWKVDCRSDSDEINCT-EICLHNEFSCNGGECIPRAY 200

Query 3593 KCDGDHDCADGSDDEKDCDCT-PRCDMDQFQCKSGHCIPLRWRCADADCMGSDDEEACGTG- 3650
           CD +DC DGSDE C P C QF C SG CI W CD + DC D DE+ C +G
Sbjct 201 VCDHDNDCCQDGSDEHACNYPTCGGYQFTCPSGRCIYQNWVCDGEDDCKDNGDEDCGCEGP 260

Query 3651 --VRTCPLDEFQC-NNTLCKPLAWKCDGEDDCGSDSDENPEECARF 3693
           V C E+ C + C + CDG DC DEN ++
Sbjct 261 HDVHKCSPREWSCPESGRCISIIYKVDGILDCPGREDENNTSTGKY 306

```



Score = 209 bits (532), Expect = 8e-51

Identities = 123/350 (35%), Positives = 166/350 (47%), Gaps = 41/350 (11%)

```

Query 3373 KCRPGQFQCSSTGICTNPAFICDGDNDCCQDSDSEANCDIHVLPSQFKCTNTNRCIPGIFR 3432
           +C F+C +G C + CDG DC D+DE C + C FKC + +CIP +
Sbjct 27 ECDSAHFRCGSGHCIPADWRCDGTkDCSDDADEIGCAVVTCCQQGYFKCQSEGCIPNSWV 86

Query 3433 CNGQDNCGDGEDER-DCPEVTCAPNQFQCSITKRCIPRVWVCDRDNCVDGSDSEPANCTQ 3491
           C+ +C DG DER DC + TC+ +Q CS +CIP + CD DC DG+DE +C
Sbjct 87 CDQDQCDGSDSDEKQDCSQSTCSSHQITCS-NGQCIPSEYRCDHVRDCPDGADE-NDQCY 144

Query 3492 MTCGVDEFRCKDSGRICIPARWKCDGEDDCGSDGSEPKKECDERTCEPY----QFRCKNNR 3547
           TC ++ C D+G C KCD + DC ++ DE C +F C N
Sbjct 145 PTC--BQLTC-DNGACYNTSQKCDWKVDC-----RSDSDEINCTEICLHNEFSCNGGE 194

Query 3548 CVPGRWQCDYDNDCGDNSDEESCTPRPCESEFSCANGRCIAGRWKCDGDHDCADGSDSEK 3607
           C+P + CD+DND D SDE +C C +F+C +GRCI W CDG+ DC D DE
Sbjct 195 CIPRAYVCDHDNDCCQDGSDEHACNYPTCGGYQFTCPSGRCIYQNWVCDGEDDCKDNGDED 254

Query 3608 DC-----TPRCMDQFQFC-KSGHCIPLRWRCADADCMGSDDEEACGTGVRTCPLDEFQ 3660
           C +C ++ C +SG CI + CD DC DE TG
Sbjct 255 GCESGPHDVHKCSPREWSCPESGRCISIIYKVDGILDCPGREDENNTSTGK-----Y 306

Query 3661 CNNTLCKPLAWKCDGEDDCGSDSDENPEECARFVCPNRPFRCKNDRVCL 3710
           C+ TLC L +C E P A F CPP + R C+
Sbjct 307 CSMTLCSAL-----NCQYQCHETPYGGACF-CPPGYIINHNSRSTCV 347

```



Score = 174 bits (440), Expect = 4e-40

Identities = 107/302 (35%), Positives = 135/302 (44%), Gaps = 55/302 (18%)

```

Query 3331 VSNCTASQFVCKND-KCIPFWKCDTEDDCGDHSDPEPPDCPEFKCRPGQFQCSTGICTNP 3389
          V C F C+++ +CIP W CD + DC D SDE DC + C Q CS G C
Sbjct 64 VVTCQQGYFKCQSEGCIPNSWVCDQDQDCDGSDEQDCSOSTCSSHQITCSNGQCIPS 123

Query 3390 AFICDGDNDQDSDNDEANCDIHVCLPSQFKCTNTNRCIPGIFRCNGQDNCGDGEDERDCP 3449
          + CD DC D +DE +C C Q C N C +C+ + +C D DE +C
Sbjct 124 EYRCDHVDPCPDGADENDCQYPTC--EQLTCDN-GACYNTSQKCDWKVDCRDSSDEINCT 180

Query 3450 EVTCAPNQFQCSITRKCRIPRVVWVCDRDNDVGSDEPANCTQMTGCVDEFRCCKDSGRICIP 3509
          E+ C N+F C CIPR +VCD DNDC DGSDE A C TCG +F C SGRCI
Sbjct 181 EI-CLHNEFSCG-NGECIPRAYVCDHDNDQDGSDEHA-CNYPTCGGYQPTC-PSGRCI- 235

Query 3510 ARWKCDGEDDCDGSDEPKECEBDEBTECEPYQFRCKNNRCPVGRWQCDYDNDGDNDSDEES 3569
          YQ W CD ++DC DN DE+
Sbjct 236 -----YQ-----NWVCDGEDDCDKNDEDEG 255

Query 3570 CTPRP-----CSESEFSC-ANGRCIAGRWKCDGDHDCADGSDSEKDCPTRCDMDQFQCKSG 3623
          C P CS E+SC +GRCI+ CDG DC DE + + C +
Sbjct 256 CESGPVHVHKCSPREWSGPCSGRCISIIYKVDGILLDCPGREDENNTSTAIGSTE-NFLIFA 315

Query 3624 HC 3625
          +C
Sbjct 316 NC 317

```



Score = 159 bits (402), Expect = 1e-35

Identities = 165/632 (26%), Positives = 240/632 (37%), Gaps = 109/632 (17%)

```

Query 3817 PGQPGCQDINECLRF-GTCSQLCNNTKGGHL--CSCARNFMKTHNTCKAEGSEYQVLYIA 3873
          P P + N CL G CS LC G H C CA +++ A +E L A
Sbjct 2335 PRSPAENVNNPCLENNGGCSHLCFALPGLHTPKDCAPFTQSDGKKAISTE-NFLIFA 2393

Query 3874 DDNEIRSL-FPGHPHSAYEQAFQGDSEVRIDAMDVHVKAAGRVIWYN--WHTGTISYRSL 3929
          N +RSL HS Q + +V ++D + R+Y+T G ISY +L
Sbjct 2394 LSNLSRLSLHLDPENHSPPFQTIINVERTVM--SLDYDSVSDRIYFTQNLASGVQGISYATL 2451

Query 3930 PPAAPPTTSNRHRQIDRGVTHLNISGLKMPRGIAIDWVAGNVYWTSDSGRVDIEVAQMKG 3989
          T + SG+ GIA DW+ +Y++D +I G
Sbjct 2452 SSGIHTPT-----VIASGIGTAGDIAFDWITRRIYYSYDLNQMINSMAEDG 2497

Query 3990 ENRKTLSIGMIDEPHAIIVVDPLRGTMYSWDGWNHPKIETAAMDGTLRETLVQDNIQWPTG 4049
          NR + + +P AIV+DP +G +YW+DW H KIE A + G R +V ++ P+G
Sbjct 2498 SNRTPI--ARVPKPRAIVLDPQGYLYWADWDTHAKIERATLGGNFRVPVIVNSSLVMPSG 2555

Query 4050 LAVDYHNERLYWADAKLSVIGSIRLNGTDPIVAADSKRGLSHPPFSIDVFEDYIYGVTYIN 4109
          L +DY + LYW DA L I L G D V ++ H F + ++ YIY
Sbjct 2556 LTLDYEEDLLYVWDASLQRIERSTLTGVDREVIVNA--AVHAFGLTLYGQYIYWTDLTY 2612

Query 4110 NRVFKIHKF-GHSPVLNLTGGLSHASDVVLYHQHKQPEVTNPCRKK--CEWLCLLSPSG 4166
          R+++ ++K+ G + T LS + +++ + NPC++ C +C P+G
Sbjct 2613 QRIYRANKYDGGSGQIAMTNNLLSQPRGINTVVKNQKQCCNNPCQFNGGCSHICAPGPN 2672

Query 4167 PVCTCPNGKRLDNGTCVPVPSPTPPDAPRPGTCNLQCFNGGSCFLNARRQPKRCQPRY 4226
          C CP+ N + R G + C NG RC
Sbjct 2673 AECQCPHE--GNWYLANNRKHCIVDNGERCASSFTCSNG-----RCISEE 2716

Query 4227 TGDKCELDQCEWHECRNGGTCAASPSGMPTRCPCGTGTPKCTQQVCAGY---CANNSTC- 4282
          KC+ D C +G S + TC PT PT C C Y C + C

```

Blast Result

```

Sbjct  2717  W--KCDND--NDCDGSDEMESVCLHTC-SPTAFT---CANGRCVQYSYRCDYNDGCG 2767

Query  4283  -----TVNQGNQPQC---RCLP-GFLGD-----RCQYRQC-SGY- 4311
              N + C RC+P F+ + C R C SGY
Sbjct  2768  DGSDEAGCLPRDCNATTEFCMNNRRCIPREFICNGVDNCHDNNTSDEKNCPRDTCQSGYT 2827

Query  4312  -CENFGTC---QMAADGSRQCRCCTAYFEGRCEVNKCS---RCLEGACVVNKQSGDVTG 4363
              C N C DG C + + C + CS +C G C+ D
Sbjct  2828  KCHNSNICIPRVYLCDGDNDCGDNSENPTYCTTHTCSSSEFQCASGRICIPQHWHYCDQET 2887

Query  4364  NCTDGRVAP-----SCLTCVGHCSNGGSC 4387
              +C D P +CL C +GG C
Sbjct  2888  DCFDASDEPASCGHSERTCLADEFKC-DGGRC 2918

```



Score = 153 bits (387), Expect = 5e-34

Identities = 89/244 (36%), Positives = 119/244 (48%), Gaps = 28/244 (11%)

```

Query  2513  DDLTCRAVNSSCRAQDEFEC-ANGECINFSLTCGVPCHKDKSDKEPSYCNRRCKKTFR 2571
              D++ C V +C+ Q F+C + G+CI S CD C D SDE+ C+ C
Sbjct  58  DEIGCAVV--TCQ-QGYFKCQSBGQCIPNSWVCDQDQDCDGSDEBQD-CSQSTCSSHQI 113

Query  2572  QCSNGRCVSNMLWLCNGADDCGDSDEIPCNKTACGVGEFRCDGTGIGNSSRCNQFVDCB 2631
              CSNG+C+ + C+ DC DG+DE C C + C +G C S +C+ VDC
Sbjct  114  TCSNGQCIPSEYRCDHVRDCPDGADENDCQYPTCE--QLTCDNGACYNTSQKCDWKVDCR 171

Query  2632  DASDEMNCSATDCSSYFRLGVKGVLFPQCERTSLCYAPSWVCDGANDCGDYSDEBDCPGV 2691
              D+SDE+NC+ + F G C ++VCD NDC D SDE C
Sbjct  172  DSSDEINCTEICLHNEFSCG-----NGECIPRAYVCDHNDQDGSDEHAC--- 217

Query  2692  KRPRCLPNYFACPSGRICIPMSWTCDEKEDDCEHGEDETHCNK-----FCSEAQFEC-QNH 2744
              P C F CPGSRCI +W CD EDDC+ DE C CS ++ C ++
Sbjct  218  NYPTCCGYQFTCPSGRCIYQNWVCDGEDDCKDNGDEDGCGESGPHDVHKCSPREWSCPESG 277

Query  2745  RCIS 2748
              RCIS
Sbjct  278  RCIS 281

```



Score = 122 bits (305), Expect = 2e-24

Identities = 99/276 (35%), Positives = 128/276 (46%), Gaps = 29/276 (10%)

```

Query  801  QVGINKCRVNNGGCSSLCLATPGSRQCAEADQVLADAGVTCLANPSYVPPPPQCPGEFA 860
              Q G KC+ + G C + C D+ D TC ++ QC P E+
Sbjct  68  QQGYFKQC-SEQQCIPNSWVCDQDQDCDGSDEBQDQCSQSTCSSHQITCSNGQCIPSEY- 125

Query  861  CANSRCIQRWKCDCGDNDCLDNSDEAPALCHQHTCPSDRFKCENNRICIPNRWLCDCGND 920
              +CD DC D +DE C TC ++ C+N C CD DC
Sbjct  126  -----RCDHVRDCPDGADEND--CQYPTC--BOLTCNGACYNTSQKCDWKVDCR 170

Query  921  GNSEDESINATCSARTCPNPQFSCASGRICIPISWTCDLDDCGDRSDESASCAYPCTFPLT 980
              +S DE N T C N+FSC +G CIP ++ CD D+DC D SDE A C YPTC
Sbjct  171  RDSSDEINCT--EICLHNEFSCGNGECIPRAYVCDHNDQDGSDEHA-CNYPTCCGY- 225

```

```

Query 981 QFTCNNGRGININWRCDNDNDGDSDEAGCS-----HSCSSTQFKC-NSGRCIPEHWT 1033
          QFTC +GRCI NW CD ++DC DN DE GC H CS ++ C SGRCI +
Sbjct 226 QFTCPSGRCIYQNWVCDGEDDCKDNGDEDGCESGPHDVHKSPREWSCPESGRCIISYKV 285
          QFTCPCSGRCIYQNWVCDGEDDCKDNGDEDGCESGPHDVHKSPREWSCPESGRCIISYKV

Query 1034 CDGDNDGCDYSDETHANCTNQATRPGGCHTDEFQC 1069
          CDG DC DE + + + ++QC
Sbjct 286 CDGILDCPGRDENNTSTGKYCSMTLCSALNCQYQC 321
          CDGILDCPGRDENNTSTGKYCSMTLCSALNCQYQC

```

Score = 119 bits (298), Expect = 1e-23
 Identities = 117/488 (23%), Positives = 191/488 (39%), Gaps = 66/488 (13%)

```

Query 3963 IAIDWVAGNVYWTDSGRDVIEVAQMKGENRKTLSIGMIDEPHAIVVDPRLRGTMYWSDWGN 4022
          +A DW++ N+YWTDS I V ++ + R+T++ ++ P ++VV P G ++++DW
Sbjct 789 LAFDWISKNLYWTDShYKISVMRLADKTRRTTVQ-YLNNPRSVVVHPPFAGYLFFTDWFR 847
          LAFDWISKNLYWTDShYKISVMRLADKTRRTTVQ-YLNNPRSVVVHPPFAGYLFFTDWFR

Query 4023 HPKIETAAMDGLTRELTVQDNIQWPTGLAVDYHNERLYWADAKLSVIGSIRLNGTDPIVA 4082
          KI A DG+ ++ + WP GLA+D+ RLYW DA I +G D
Sbjct 848 PAKIMRAWSDGSHLLPVIINTTLGWPNGLAIDWAASRLYWDVYFDKIEHSTFDGLDRRL 907
          PAKIMRAWSDGSHLLPVIINTTLGWPNGLAIDWAASRLYWDVYFDKIEHSTFDGLDRRL

Query 4083 ADSKRLGSHPPFSIDVFEDIYIGVTYINNRFVKIHKFGHSPLVNLTGGLSHASDVVLYHQH 4142
          ++ ++HPPF + +F +++ + + ++ K + + G+++ + Y +
Sbjct 908 GHIEQ-MTHPFGLAIFGEHLFFTDWRLGAIIRVRKADGGEMTVIRSGIAYILHLKSYDVN 966
          GHIEQ-MTHPFGLAIFGEHLFFTDWRLGAIIRVRKADGGEMTVIRSGIAYILHLKSYDVN

Query 4143 KQPEVTNPCDRK-----KCEWLCLLSPS-GPVCTCPNGKRLDNGTCVPVPSPTPPDAPR 4196
          Q +N C++ C C P+ VC CP G RL + PT P +
Sbjct 967 IQTG-SNACNQPTHFNGDCSHFCFPVPNFQRCVCGCPYGMRLASNHLTCEGDPTNEPPTQ 1025
          IQTG-SNACNQPTHFNGDCSHFCFPVPNFQRCVCGCPYGMRLASNHLTCEGDPTNEPPTQ

Query 4197 PGTCNLQCFNGGSCFLNARRQPKRCQPRYTGDKE-LDQCWEHCRN-----GGTCAAS 4249
          G + C NG RC P Y C+ +D C ++ TC++S
Sbjct 1026 CGLFSPFCKNG-----RCVPNY--LCDGVDDCHDSDQLCGTLNNTCSSS 1070
          CGLFSPFCKNG-----RCVPNY--LCDGVDDCHDSDQLCGTLNNTCSSS

Query 4250 --PSGMPT-----RCPTGFTGPKCTQVQVAGYCANNSTCTVNGNQPPQCRC-L 4295
          G C C G C A TC +Q C
Sbjct 1071 AFTCGHGECEPAHWRCDKRNDVDSDEHNCPTHAPASCLDTQYTCNDNHQCSISKNWVCDT 1130
          AFTCGHGECEPAHWRCDKRNDVDSDEHNCPTHAPASCLDTQYTCNDNHQCSISKNWVCDT

Query 4296 PGFLGDRQCQYRCQSGYCEFGTCQMAADGSRQCRCTAYFEGSRCEVKNKSRCLEGA---- 4351
          GD + C+ + TCQ + RC C+ +K C++G+ C
Sbjct 1131 DNDGCGDSDEKNCN----STETCQSPQFNCNPHRCIDL--SFVCDGDK--DCVDGSDSDEVG 1182
          DNDGCGDSDEKNCN----STETCQSPQFNCNPHRCIDL--SFVCDGDK--DCVDGSDSDEVG

Query 4352 CVVNKQSGDVTNCNTDGRVAPSLCTCVGHCSNGGSCMTNSKMMPECQCPHMTGPRCEEH 4411
          CV+N + C D C+ C C+ NS E CP M G C
Sbjct 1183 CVLNCASQFCKASGD----KCIGVTNRCDGVFDCSDNS--DEAGCPTRPPG-MCHSD 1233
          CVLNCASQFCKASGD----KCIGVTNRCDGVFDCSDNS--DEAGCPTRPPG-MCHSD

Query 4412 VFSQQQPG 4419
          F Q+ G
Sbjct 1234 EFQCEQEDG 1241
          EFQCEQEDG

```

Score = 104 bits (259), Expect = 4e-19
 Identities = 61/180 (33%), Positives = 84/180 (46%), Gaps = 21/180 (11%)

```

Query 3297 NNGGCSNLCLLSPGGGHHKACPTNFYLGSDGRCTVSNCTASQFVCKNDKICPFWKCDTE 3356
          +NG C N KC + SD C C ++F C N +CIP + CD +

```

Blast Result

```

Sbjct 153 DNGACYNT-----SQKCDWKVDCRDSSDEINCTEICLHNEFSCGNCECIPRAYVCDHD 205

Query 3357 DDCGDHSDEPPDCPEFKCRPGQFCSTGICTNPAFICDGDNDQDNSDEANC-----DIH 3411
+DC D SDE C C QF C +G C ++CDG++DC+DN DE C D+H
Sbjct 206 NDCQDGSDEHA-CNYPTCGGYQFTCPSGRCIYQNWVCDGEDDCKDNGDEDGECESGPHDVH 264

Query 3412 VCLPSQFKCTNTNRCIPGIFRCNGQDNCGDGEDERD-----CPEVTCAP--NQFQCSIT 3463
C P + C + RCI C+G +C EDE + C C+ Q+QC T
Sbjct 265 KCSPREWSCPSGRCISYKVCDDILDCPGREDENNTSTGKYCSMTLCSALNCQVQCHET 324

```



Score = 94.0 bits (232), Expect = 5e-16
 Identities = 75/261 (28%), Positives = 98/261 (37%), Gaps = 36/261 (13%)

```

Query 2490 QDLCLLTHQHVNCSGRGRILQDDLTCRAVNSSCRAQDEFECA-----NGECIN 2539
QD T H +C G+ + + C V DE +C NG C N
Sbjct 101 QDCQSCSSH-QITCSNGQCIPSEYRCDHVRDCPDGADENDCQYPTCEQLTCDNGACYN 159

Query 2540 FSLTCDGVPHCKDKSDEKPSYCNRRCKKTRQCSNGRCVSNMLWCNGADDGSDGSDIIP 2599
S CD C+D SDE + C C NG C+ C+ +DC DGSDE
Sbjct 160 TSQKCDWKVDCRDSSDEINC---TEICLHNEFSCGNCECIPRAYVCDHDNDQDGSDEHA 216

Query 2600 CNKTACGVGEFRCDGTGIGNSSRCNQFVDCEDASDEMNCSATDCSSYFRLGVKGVLFQP 2659
CN CG +F C G CI + C+ DC+D DE C S +
Sbjct 217 CNYPTCGGYQFTCPSGRCIYQNWVCDGEDDCKDNGDEDGCE----SGPHDVHKCSPREWS 272

Query 2660 CERTSLCYAPSWVCDGANDCGDYSDERDCPGVK-----RPRCPLNYFA----C 2703
C + C + VCDG DC DE + K + +C + C
Sbjct 273 CPESGRCISYKVCDDILDCPGREDENNTSTGKYCSMTLCSALNCQYQCHETPYGGACFC 332

Query 2704 PSGRCIPM--SWTCDKEDDCE 2722
P G I S TC + DDC+
Sbjct 333 PPGYIINHNSRTCVEFDCCQ 353

```



Score = 78.6 bits (192), Expect = 2e-11
 Identities = 46/109 (42%), Positives = 57/109 (52%), Gaps = 10/109 (9%)

```

Query 23 APKTCSPKQFACRDQITCISKGWRCDGERDCPDGSDEAPEICPQSKAQRCQP-NEHNCLG 81
A +TC P QF C + CI + W+CD + DC D SDE E C S A C E +C
Sbjct 3631 ASRTCPRGQFRCANG-RCIPQAWKCDVDNDCGDHSDIEEC-MSSAHLCDNFTEFSCKT 3688

Query 82 TELCVPMRLCNGVQDCMDGSDGPHCRELQGNCSRLG---CQ-HHCVP 126
C+P +CNGV DC D SDE C E C +G C+ HHC+P
Sbjct 3689 NYRICKWAVCNGVDDCRDNDSE-QGCEE--RTCHPVGDFRCKNHHCIP 3734

```



Score = 78.2 bits (191), Expect = 3e-11
 Identities = 93/430 (21%), Positives = 162/430 (37%), Gaps = 72/430 (16%)


```

Query 25      KTCSPKQFACRDQITCISKGWRCGERDCPDGSDEAPEICPQSKAQRCPNEHNCLGTE- 83
+TC +F C D CI W CDG+ DC D SDE Q + Q C +E C+
Sbjct 2904    RTCLADEFKC-DGGRCIPSEWICDGDNDGDMSEDEKR--HQCNQNCSDSEFLCVNDRP 2960

Query 84      ---LCVPMSRLCNGVQDCMDGSDEGPHCRELQGNCSRLGCQHH-CVPTLDGPTCYCNSSF 139
+C P S +C+G DC DG DE +C + + C + C+P + C ++
Sbjct 2961    PDRCRIPQSWVCDGVDCTDGYDENQNCNCTRRTCSENEFTCGYGLCIPKIF--RCDRHNDC 3018

Query 140     QLQADGKTCKDFDECSVYGTCQ---LCTN---TDGSFIC----GCVGEG----YLLQPD 184
+D + C +Y TC Q C N +F+C C +G +L
Sbjct 3019    GDYSDERGC-----LYQTCQQNQFTCQNGRCISKTFVCEBDNDGCGSDELMHLCHTP 3071

Query 185     NRSCKAKNEPVRPPVLLIANSQNILATYLSGAQVSTITPTSTRQTTAMDFSANETVCW 244
+C D + + N L L + + +
Sbjct 3072    EPTCPPEHFKCDNGRCIEMMKLCNHLDDCLDNDSEKCGGINECH-----DPSISG 3121

Query 245     VHVGDSSAAQTQLKCARMPGLKGFVDEHT---INISLSLHHVQMAIDWLGNFY----- 295
+ T C+ PG K D+ T I+ + V + + G++
Sbjct 3122    CDHNCTDTLTFSYFCSCRPGYKLMSDKRCTVDIDECTEMPFCVSKCENVIGSYICKCAPG 3181

Query 296     FVDDIDDRIFVFNCRNGDTCVTLLDLELYNPKGIALD-----PAMKGVFFTDYQGIPK 347
++ + D + C +N + L+ Y + + +D + V D+ ++ K
Sbjct 3182    YLREPDGK--TCRQNSNIEPYLIFSNRYLRNLIDGYFYSILBGLDNVVALDFDRVEK 3239

Query 348     -----VERCDMDGQNRKTLVDSKIVFPHGITLDDLVSRLVYWADAYLDYIEVVYD 396
+ER ++ N+ +++ ++ + +D VSR +YW DA LD + V D
Sbjct 3240    RLYWIDTQRQVIERMFLNKTNKETIINHRLPAAESLAVDWVSRKLYWLDARLDGFLVSD 3299

Query 397     EGKGRQTIQ 406
G R+ + Q
Sbjct 3300    NGGHRRLAQ 3309

```



Score = 73.2 bits (178), Expect = 9e-10
 Identities = 44/170 (31%), Positives = 63/139 (45%), Gaps = 26/139 (18%)

```

Query 22      DAPKTCSPKQFACRDQITCISKGWRCGERDCPDGSDEAPEICPQSKAQRCPNEHNCLG 81
++ +TC P QF C + CI + CDG++DC DGSDE + C ++ C
Sbjct 1144    NSTETCQPSQFNCNPNH-RCIDLFSFVCDGDKDCVDGSDVGVCL-----NCTASQFKCAS 1196

Query 82      TELCVMSRLCNGVQDCMDGSDEGPHCRELQGNCSRLGCQHHCVPTLDGPTCYCNSSFQ 141
+C+ ++ C+G+ DC D SDE GC PT C+ + FQ
Sbjct 1197    GDKICIGVTNRCDGVFDCSDNSDEA-----GC-----PTRPPGMCH-SDEFQC 1237

Query 142     QADGKTCKDFDECSVYGTC 160
Q DG +F EC + C
Sbjct 1238    QEDGICIPNFWBCDGHDPDC 1256

```

Score = 72.8 bits (177), Expect = 1e-09
 Identities = 54/170 (31%), Positives = 77/170 (45%), Gaps = 39/170 (22%)

Query 26 TCSPKQFACRDQITCISKGWRCGERDCPDGSDEAPEICPQSKAQRCPNEHNCLGTCLC 85

```

TC   F C + + CI   W CD ++DC DGSDE + C QS   C ++ C + C
Sbjct 66 TCQQGYFKCQSEGCIPNSWVCDQDQDCDDGSDERQD-CSQS---TCSSHQITCSNGQ-C 120

Query 86 VPMSRLCNGVQDCMDGSDEG----PHCRELQGNCSRLGCQHHCVPTLDGPTCYCNSSFQ 141
      +P   C+ V+DC DG+DE   P C +L   T D   CY S
Sbjct 121 IPSEYRCDHVRDCPDGADENDCQYPTCEQL-----TCDNGACYNTSQ--- 162

Query 142 QADGKT-CKD-FDECSVYGTCSQLCTNTDGSFICG---CV-EGYLLQPDN 185
      + D K C+D DE +   C+++C + + F CG   C+ Y+ DN
Sbjct 163 KCDWKVDCRDSSDEIN---CTEICLHNE--FSCGNCECIPRAYVCDHDN 206

```



Score = 69.7 bits (169), Expect = 1e-08

Identities = 52/165 (31%), Positives = 69/165 (41%), Gaps = 20/165 (12%)

```

Query 21 IDAPKTCSPKQFACRDQITCISKGWRCDDGERDCPDGSDEAPEICPQSKAQRCPNEHNCL 80
      +D + C   F C +   CIS+ W+CD + DC DGSDE +C   C P C
Sbjct 2694 VDNGERCGASSFTCSNG-RCISEEWKCDNDNDCGDSDEMESVC---ALHTCSPTAFTCA 2749

Query 81 GTELCVPMRLCNGVQDCMDGSDE-GPHCRELQGNCSRLGCQHHCVPTLDGPTCYC 135
      CV S C+   DC DGSDE G R+   +   C+P   +G C+
Sbjct 2750 NGR-CVQYSYRCDYYNDCGDSDEAGCLFRDCNATTEFCMCNRRRCIPREFICNGVDNCHD 2808

Query 136 NSSFQLQADGKTCKDFDECSVYGTG--SQLCTN----TDGSFICG 174
      N++   +D K C D   S Y C S +C   DG CG
Sbjct 2809 NNT----SDEKNCPRDTCQSGYTKCHNSNICIPRVYLCDGDNDGC 2849

```



Score = 64.7 bits (156), Expect = 3e-07

Identities = 44/149 (29%), Positives = 60/149 (40%), Gaps = 13/149 (8%)

```

Query 25 KTCSPKQFACRDQITCISKGWRCDDGERDCPDGSDEAPEICPQSKAQRCPNEHNCLGT 84
      +TC   C +   CI + + CDG+ DC D SDE P C   C +E C +
Sbjct 2820 RTCQSGYTKCHNSNICIPRVYLCDGDNDGCNDSDENFTYC---THTCSSEFQC-ASGR 2875

Query 85 CVPMRLCNGVQDCMDGSDEGPHCRELQGNCSRLGCQHHCVPTLDGPTCYCNSSFQ 144
      C+P   C+   DC D SDE   C +   C L + C   DG C S + D
Sbjct 2876 CIPQHWYCDQETDCFDASDEPASCCHSERTC--LADEFKC----DGGRC-IPSEWICDGD 2928

Query 145 GKTKCKDFDECSVYGTCSQLCTNTDGSFIC 173
      DE   +   +Q C +D F+C
Sbjct 2929 NDCGDMSDEDKRHQCNQNC--SDSEFLC 2955

```



Score = 60.8 bits (146), Expect = 5e-06

Identities = 36/113 (31%), Positives = 47/113 (41%), Gaps = 20/113 (17%)

```

Query 23 APKTCSPKQFACRDQITCISKGWRCDDGERDCPDGSDEAPEICPQSKAQRCPNEHNCLGT 82
      AP+ C+ +F C +Q CI   W CD   DC D SDE   + + C P C

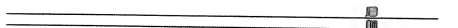
```

Blast Result

Sbjct 3755 APRECTESEFRCVNQ-QCIPSRWICDHYNDCGDNSEDER-----DCEMRTCHPEYFQCTSG 3808

Query 83 ELCVPMSRLCNGVQDCMDGSDSDE-----GPHCRELQGNCSRLGCQHHCVP I26
 CV C+G DC+D SDE G +C+ C H C+P

Sbjct 3809 H-CVHSELKCDGSADCLDASDEADCPTRFPDGAYCQATMFECK----NHVCIP 3856



Score = 57.8 bits (I38), Expect = 4e-05
 Identities = 31/81 (38%), Positives = 43/81 (53%), Gaps = 8/81 (9%)

Query 25 KTCSPK-QFACRDQITCISKGWRCDCGERDCPDGSDEAPEICPQSKAQRCQPNEHNCGLTE 83
 +TC P F C++ CI W+CDG+ DC D SDE E C + C +E C+ +

Sbjct 3717 RTCHPVGDFRCKNH-HCIPLRWQCDGQNDGDNSE--ENC---APRECTESEFRCVNQQ 3770

Query 84 LCVPMMSRLCNGVQDCMDGSDSDE 104
 C+P +C+ DC D SDE

Sbjct 3771 -CIPSRWICDHYNDCGDNSE 3790

CPU time: 0.08 user secs. 0.05 sys. secs 0.13 total secs.